

## SEQUENCE LISTING

<110> SmithKline Beecham Biologicals

<120> Novel compounds

<130> BM45311

<160> 14

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 519

<212> DNA

<213> Bacteria

<400> 1

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| acaggctgtg ccaataaaatc aacaagtcaa gtatggttg ctcctaattgc acccacaggt  | 120 |
| tacactgggg ttatctatac tggtgttgca cctttggtag ataatgatga gaccgttaag   | 180 |
| gctctggcaa gcaagctacc cagttgggtt tattttgact ttgattctga tgagattaaa   | 240 |
| ccgcaagctg ctgccatctt agacgaacaa gcacaatttt taaccaccaa tcaaacagct   | 300 |
| cgtgtttgg ttgcagggtca taccgatgag cgtggtagtc gtgagttataa tatgtcaactg | 360 |
| ggggaaacgcc gtgcgggtggc ggtacgcaac tatttgcttg gtaaaggcat taatcaagcc | 420 |
| agcgttgaga ttatcagttt tggtaagaa cgcctatcg catttggcac aaatgaagaa     | 480 |
| gcatggtcac aaaatcgtcg tgctgaactg tcttattaa                          | 519 |

<210> 2

<211> 172

<212> PRT

<213> Bacteria

<400> 2

Met Met Leu His Ile Gln Ile Ala Ala Ala Ala Ala Ala Leu Ser Val

1

5

10

15

Leu Thr Phe Met Thr Gly Cys Ala Asn Lys Ser Thr Ser Gln Val Met  
           20                  25                  30  
 Val Ala Pro Asn Ala Pro Thr Gly Tyr Thr Gly Val Ile Tyr Thr Gly  
           35                  40                  45  
 Val Ala Pro Leu Val Asp Asn Asp Glu Thr Val Lys Ala Leu Ala Ser  
           50                  55                  60  
 Lys Leu Pro Ser Leu Val Tyr Phe Asp Phe Asp Ser Asp Glu Ile Lys  
   65                  70                  75                  80  
 Pro Gln Ala Ala Ala Ile Leu Asp Glu Gln Ala Gln Phe Leu Thr Thr  
           85                  90                  95  
 Asn Gln Thr Ala Arg Val Leu Val Ala Gly His Thr Asp Glu Arg Gly  
           100                  105                  110  
 Ser Arg Glu Tyr Asn Met Ser Leu Gly Glu Arg Arg Ala Val Ala Val  
           115                  120                  125  
 Arg Asn Tyr Leu Leu Gly Lys Gly Ile Asn Gln Ala Ser Val Glu Ile  
           130                  135                  140  
 Ile Ser Phe Gly Glu Arg Pro Ile Ala Phe Gly Thr Asn Glu Glu  
   145                  150                  155                  160  
 Ala Trp Ser Gln Asn Arg Arg Ala Glu Leu Ser Tyr  
           165                  170

<210> 3  
 <211> 519  
 <212> DNA  
 <213> Bacteria

<400> 3

|   |     |
|---|-----|
| atgatgttac atattcaaat tgccggcgct gccggcgctt tatcggtact aacttttatg   | 60  |
| acaggctgtg ccaataaatac aacaagtcaa gttatggttg ctccataatgc acccacaggt | 120 |
| tacactgggg ttatctatac tggtgttgc accttggtag ataatgatga gaccgttaag    | 180 |
| gctctagcaa gcacgctacc cagtttggtt tatttgact ttgattctga tgagattaaa    | 240 |
| ccgcaagctg ctgccatctt agacgaacaa gcacaatttt taaccaccaa tcaaaacagct  | 300 |
| cgtgtttgg ttgcaggtca taccgatgag cgtggtagtc gtgagtataa tatgtcactg    | 360 |
| ggggAACGTC gtgcgggtggc ggtacgcaac tatttgcttg gtAAAGGcat taatcaAGCC  | 420 |
| agcgttgaga ttatcagttt tggtaagaa cggcctatcg catttggcac aaatgaagaa    | 480 |
| gcatggtcac aaaatcgtcg tgctgaactg tcttattaa                          | 519 |

<210> 4

<211> 172

&lt;212&gt; PRT

&lt;213&gt; Bacteria

&lt;400&gt; 4

Met Met Leu His Ile Gln Ile Ala Ala Ala Ala Ala Ala Leu Ser Val  
 1 5 10 15  
 Leu Thr Phe Met Thr Gly Cys Ala Asn Lys Ser Thr Ser Gln Val Met  
 20 25 30  
 Val Ala Pro Asn Ala Pro Thr Gly Tyr Thr Gly Val Ile Tyr Thr Gly  
 35 40 45  
 Val Ala Pro Leu Val Asp Asn Asp Glu Thr Val Lys Ala Leu Ala Ser  
 50 55 60  
 Thr Leu Pro Ser Leu Val Tyr Phe Asp Phe Asp Ser Asp Glu Ile Lys  
 65 70 75 80  
 Pro Gln Ala Ala Ala Ile Leu Asp Glu Gln Ala Gln Phe Leu Thr Thr  
 85 90 95  
 Asn Gln Thr Ala Arg Val Leu Val Ala Gly His Thr Asp Glu Arg Gly  
 100 105 110  
 Ser Arg Glu Tyr Asn Met Ser Leu Gly Glu Arg Arg Ala Val Ala Val  
 115 120 125  
 Arg Asn Tyr Leu Leu Gly Lys Gly Ile Asn Gln Ala Ser Val Glu Ile  
 130 135 140  
 Ile Ser Phe Gly Glu Arg Pro Ile Ala Phe Gly Thr Asn Glu Glu  
 145 150 155 160  
 Ala Trp Ser Gln Asn Arg Arg Ala Glu Leu Ser Tyr  
 165 170

&lt;210&gt; 5

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Bacteria

&lt;400&gt; 5

|  |     |
|--|-----|
| atgatgttac atattcaaat tgccggcgct gcccggcgtt tatcggtact aacttttatg  | 60  |
| acaggctgtg ccaataaaatc aacaagtcaa gttatggttg ctcctaatgc acccacaggt | 120 |
| tacactgggg ttatctatac tggtgttgca cctttggtag ataatgatga gactatcaag  | 180 |
| actttggcaa gcacgctacc cagttgggtt tatttgact ttgattctga tgagattaaa   | 240 |
| ccgcaagctg ctgccatctt agacgaacaa gcacaattt taaccaccaa tcaaacagct   | 300 |
| cgtgtttgg ttgcaggtca taccgatgag cgtggtagtc gtgagtataa tatgtcactg   | 360 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| ggggAACGCC | gtgcGGTGGC | ggtaCGCAAC | tatTTGCTTG | gtAAAGGCAT | taATCAAGCC | 420 |
| agcgTTgaga | ttatcAGTT  | tggtGAAGAA | cGCCCTATCG | cattTGGCAC | aaATGAAGAA | 480 |
| gcATGGTCAC | aaaATCGTCG | tgctGAACTG | tcttATTAA  |            |            | 519 |

<210> 6  
<211> 172  
<212> PRT  
<213> Bacteria

<400> 6

|   |                 |     |     |     |
|---|-----------------|-----|-----|-----|
| Met Met Leu His Ile Gln Ile Ala Ala Ala Ala Ala     | Leu Ser Val     |     |     |     |
| 1   | 5               | 10  | 15  |     |
| Leu Thr Phe Met Thr Gly Cys Ala Asn Lys Ser Thr     | Ser Gln Val Met |     |     |     |
| 20  |                 | 25  | 30  |     |
| Val Ala Pro Asn Ala Pro Thr Gly Tyr Thr Gly Val     | Ile Tyr Thr Gly |     |     |     |
| 35  |                 | 40  | 45  |     |
| Val Ala Pro Leu Val Asp Asn Asp Glu Thr Ile Lys     | Thr Leu Ala Ser |     |     |     |
| 50  |                 | 55  | 60  |     |
| Thr Leu Pro Ser Leu Val Tyr Phe Asp Phe Asp Ser Asp | Glu Ile Lys     |     |     |     |
| 65  |                 | 70  | 75  | 80  |
| Pro Gln Ala Ala Ala Ile Leu Asp Glu Gln Ala Gln     | Phe Leu Thr Thr |     |     |     |
| 85  |                 | 90  | 95  |     |
| Asn Gln Thr Ala Arg Val Leu Val Ala Gly His Thr Asp | Glu Arg Gly     |     |     |     |
| 100   |                 | 105 | 110 |     |
| Ser Arg Glu Tyr Asn Met Ser Leu Gly Glu Arg Arg     | Ala Val Ala Val |     |     |     |
| 115   |                 | 120 | 125 |     |
| Arg Asn Tyr Leu Leu Gly Lys Gly Ile Asn Gln Ala     | Ser Val Glu Ile |     |     |     |
| 130   |                 | 135 | 140 |     |
| Ile Ser Phe Gly Glu Glu Arg Pro Ile Ala Phe Gly     | Thr Asn Glu Glu |     |     |     |
| 145   |                 | 150 | 155 | 160 |
| Ala Trp Ser Gln Asn Arg Arg Ala Glu Leu Ser Tyr     |                 |     |     |     |
| 165   |                 | 170 |     |     |

<210> 7  
<211> 519  
<212> DNA  
<213> Bacteria

<400> 7

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|--|-----|
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| acaggctgtg ccaataaaatc aacaagtcaa gttatggttg ctcctaatgc acccacgggt | 120 |
| tacgctggcg ttatctacac tggtgttgca cctttggtag ataatgatga gaccgtcaag  | 180 |
| gctttggcaa gcacgctacc cagtttggtt tattttgact ttgattctga tgagattaaa  | 240 |
| ccgcaagctg ctgccatctt agacgaacaa gcacaatttt taaccaccaa tcaaacagct  | 300 |
| cgtgttttgg ttgcaggtca taccgatgag cgtggtagtc gtgagttaa tatgtcaactg  | 360 |
| ggggAACGCC gtgcgggtgc ggtacgcaac tatttgctta gtaaaggcat caatcaagcc  | 420 |
| agcgttgaga ttatcagttt tggtgaagaa cgccctatcg catttggcac aaatgaagaa  | 480 |
| gcatggtcac aaaatcgtcg tgctgaactg tcttattaa                         | 519 |

<210> 8

<211> 172

<212> PRT

<213> Bacteria

<400> 8

|   |     |     |     |
|---|-----|-----|-----|
| Met Met Leu His Ile Gln Ile Ala Ala Ala Ala Ala Ala Leu Ser Val |     |     |     |
| 1   | 5   | 10  | 15  |
| Leu Thr Phe Met Thr Gly Cys Ala Asn Lys Ser Thr Ser Gln Val Met |     |     |     |
| 20  | 25  | 30  |     |
| Val Ala Pro Asn Ala Pro Thr Gly Tyr Ala Gly Val Ile Tyr Thr Gly |     |     |     |
| 35  | 40  | 45  |     |
| Val Ala Pro Leu Val Asp Asn Asp Glu Thr Val Lys Ala Leu Ala Ser |     |     |     |
| 50  | 55  | 60  |     |
| Thr Leu Pro Ser Leu Val Tyr Phe Asp Phe Asp Ser Asp Glu Ile Lys |     |     |     |
| 65  | 70  | 75  | 80  |
| Pro Gln Ala Ala Ala Ile Leu Asp Glu Gln Ala Gln Phe Leu Thr Thr |     |     |     |
| 85  | 90  | 95  |     |
| Asn Gln Thr Ala Arg Val Leu Val Ala Gly His Thr Asp Glu Arg Gly |     |     |     |
| 100   | 105 | 110 |     |
| Ser Arg Glu Tyr Asn Met Ser Leu Gly Glu Arg Arg Ala Val Ala Val |     |     |     |
| 115   | 120 | 125 |     |
| Arg Asn Tyr Leu Leu Ser Lys Gly Ile Asn Gln Ala Ser Val Glu Ile |     |     |     |
| 130   | 135 | 140 |     |
| Ile Ser Phe Gly Glu Glu Arg Pro Ile Ala Phe Gly Thr Asn Glu Glu |     |     |     |
| 145   | 150 | 155 | 160 |
| Ala Trp Ser Gln Asn Arg Arg Ala Glu Leu Ser Tyr                 |     |     |     |
| 165   | 170 |     |     |

<210> 9  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer sequence

<400> 9  
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21

<210> 10  
<211> 19  
<212> DNA  
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<220>  
<223> Primer sequence

<400> 10  
ggcagagtga atcttaagc

19

<210> 11  
<211> 59  
<212> DNA  
<213> Artificial Sequence

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<223> Oligonucleotide

<400> 11  
aagggcccaa ttacgcagag gggatccaat aaatcaacaa gtcaagttat gggtgctcc 59

<210> 12  
<211> 65  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide

&lt;400&gt; 12

aaggggccaa ttacgcagag ggtcgactta ttaataagac agttcagcac gacgatttg tgacc 65

&lt;210&gt; 13

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; peptide

&lt;400&gt; 13

Cys Asn Glu Glu Ala Trp Ser Gln Asn Arg Arg Ala Glu Leu Ser Tyr

1

5

10

15

&lt;210&gt; 14

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; peptide

&lt;400&gt; 14

Tyr Thr Gly Val Ala Pro Leu Val Asp Asn Asp Glu Thr Val

1

5

10

**SEQUENCE INFORMATION****BASB019 Polynucleotide and Polypeptide Sequences****SEQ ID NO:1**

*Moraxella catarrhalis* BASB019 polynucleotide sequence from strain MC2931

ATGATGTTACATATTCAAATTGCCGCCGTGCCGCCGCTTATCGGTACTAACCTTTAT  
GACAGGCTGTGCCAATAAAATCAACAAGTCAAGTTATGGTTGCTCCTAATGCACCCACAG  
GTTACACTGGGGTTATCTATACTGGTGTGCACCTTGTTAGATAATGATGAGACCGTT  
AAGGCTCTGGCAAGCAAGCTACCCAGTTGGTTATTTGACTTGATTCTGATGAGAT  
TAAACCGCAAGCTGCTGCCATCTTAGACGAACAAGCACAATTAAACCACCAATCAA  
CAGCTCGTGTGGTGCAGGTACATACCGATGAGCGTGGTAGTCGTGAGTATAATATG  
TCACTGGGGAAACGCCGTGCGGTGGCGGTACGCAACTATTCGTTGGTAAAGGCATTAA  
TCAAGCCAGCGTTGAGATTATCAGTTGGTGAAGAACGCCCTATCGCATTGGCACAA  
ATGAAGAACGATGGTCACAAATCGTCGTGCTGAACGTCTTATTAA

**SEQ ID NO:2**

*Moraxella catarrhalis* BASB019 polypeptide sequence from strain MC2931

MMLHIQIAAAAALSVLTFMTGCANKSTSQMVAPNAPTYGVIVYTGVAPLVDNDETV  
KALASKLPSLVFDSDIEKPQAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM  
SLGERRAVAVRNLYLLKGKINQASVEIISFGEERPIAFGTNEEAWSQNRRAEWSY

**SEQ ID NO:3**

*Moraxella catarrhalis* BASB019 polynucleotide sequence from strain Mcat 2911

ATGATGTTACATATTCAAATTGCCGCCGTGCCGCCGCTTATCGGTACTAACCTTTAT  
GACAGGCTGTGCCAATAAAATCAACAAGTCAAGTTATGGTTGCTCCTAATGCACCCACAG  
GTTACACTGGGGTTATCTATACTGGTGTGCACCTTGTTAGATAATGATGAGACCGTT  
AAGGCTCTAGCAAGCACGCTACCCAGTTGGTTATTTGACTTGATTCTGATGAGAT  
TAAACCGCAAGCTGCTGCCATCTTAGACGAACAAGCACAATTAAACCACCAATCAA  
CAGCTCGTGTGGTGCAGGTACATACCGATGAGCGTGGTAGTCGTGAGTATAATATG  
TCACTGGGGAAACGTCGTGCGGTGGCGGTACGCAACTATTCGTTGGTAAAGGCATTAA  
TCAAGCCAGCGTTGAGATTATCAGTTGGTGAAGAACGCCCTATCGCATTGGCACAA  
ATGAAGAACGATGGTCACAAATCGTCGTGCTGAACGTCTTATTAA

**SEQ ID NO:4**

*Moraxella catarrhalis* BASB019 polypeptide sequence from strain Mcat 2911

MMLHIQIAAAAALSVLTFCMTGCANKSTSQVMVAPNAPTYGVIYTGVAPLVDNDETV  
KALASTLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM  
SLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELEY

**SEQ ID NO:5**

*Moraxella catarrhalis* BASB019 polynucleotide sequence from strain Mcat 2960

ATGATGTTACATATTCAAATTGCCGCCGCTGCCGCCGCTTATCGGTACTAACCTTTAT  
GACAGGCTGTGCCAATAATCAACAAGTCAAGTTATGGTTGCTCCTAATGCACCCACAG  
GTTACACTGGGTTATCTATACGGTGTGACCTTGTTAGATAATGATGAGACTATC  
AAGACTTGGCAAGCACGCTACCCAGTTGGTTATTTGACTTGATTCTGATGAGAT  
TAAACCGCAAGCTGCTGCCATCTTAGACGAACAAGCACAATTAAACCACCAATCAA  
CAGCTCGTGTGGTGCAGGTACATACCGATGAGCGTGGTAGTCGTGAGTATAATATG  
TCACTGGGGAAACGCCGTGCGGTGGCGGTACGCAACTATTGCTGGTAAAGGCATTAA  
TCAAGCCAGCGTTGAGATTATCAGTTGGTGAAGAACGCCCTATCGCATTGGCACAA  
ATGAAGAACGATGGTCACAAATCGTCGTGCTGAACGTCTTATTAA

**SEQ ID NO:6**

*Moraxella catarrhalis* BASB019 polypeptide sequence from strain Mcat 2960

MMLHIQIAAAAALSVLTFCMTGCANKSTSQVMVAPNAPTYGVIYTGVAPLVDNDETI  
KTLASTLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM  
SLGERRAVAVRNYLLGKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAELEY

**SEQ ID NO:7**

*Moraxella catarrhalis* BASB019 polynucleotide sequence from strain Mcat 2969

ATGATGTTACATATTCAAATTGCCGCCGCTGCCGCCGCTTATCGGTACTAACCTTTAT  
GACAGGCTGTGCCAATAATCAACAAGTCAAGTTATGGTTGCTCCTAATGCACCCACGG  
GTTACGCTGGCGTTATCTACACTGGTGTGACCTTGTTAGATAATGATGAGACCGTC  
AAGGCTTGGCAAGCACGCTACCCAGTTGGTTATTTGACTTTGATTCTGATGAGAT  
TAAACCGCAAGCTGCTGCCATCTTAGACGAACAAGCACAATTAAACCACCAATCAA  
CAGCTCGTGTGGTGCAGGTACATACCGATGAGCGTGGTAGTCGTGAGTATAATATG  
TCACTGGGGAAACGCCGTGCGGTGGCGGTACGCAACTATTGCTTAGTAAAGGCATCAA  
TCAAGCCAGCGTTGAGATTATCAGTTGGTGAAGAACGCCCTATCGCATTGGCACAA  
ATGAAGAACGATGGTCACAAATCGTCGTGCTGAACGTCTTATTAA

**SEQ ID NO:8**

*Moraxella catarrhalis* BASB019 polypeptide sequence from strain Mcat 2969

MMLHIQIAAAAALSVLTFMTGCANKSTSQVMVAPNAPTYAGVIYTGVAPLVDNDETV  
KALASTLPSLVYFDFDSDEIKPQAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM  
SLGERRAVAVRNYLLSKGINQASVEIISFGEERPIAFGTNEEAWSQNRRAEWSY

**SEQ ID NO:9**

CCC TTA TTA ATT GAC AAT CAC

**SEQ ID NO:10**

GGC AGA GTG AAT CTT AAG C

**SEQ ID NO:11**

AAG GGC CCA ATT ACG CAG AGG GGA TCC AAT AAA TCA ACA AGT CAA  
GTT ATG GTT GCT CC

**SEQ ID NO:12**

AAG GGC CCA ATT ACG CAG AGG GTC GAC TTA TTA ATA AGA CAG TTC  
AGC ACG ACG ATT TTG TGA CC

**SEQ ID NO:13**

CNEEAWSQNRRAEWSY

**SEQ ID NO:14**

YTGVAPLVDNDETV